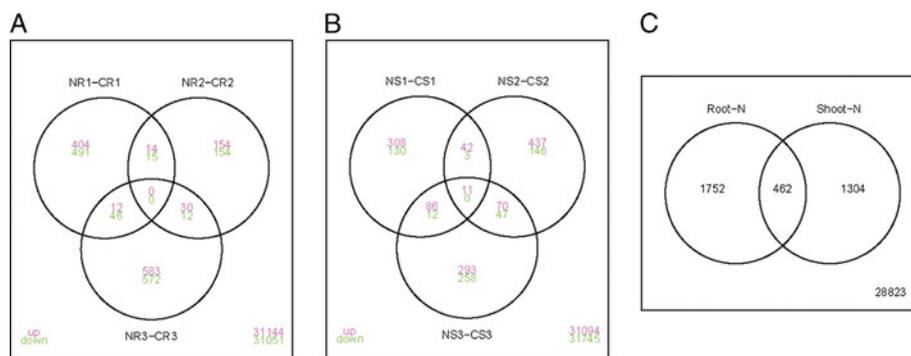


Transcriptome response to nitrogen starvation in rice

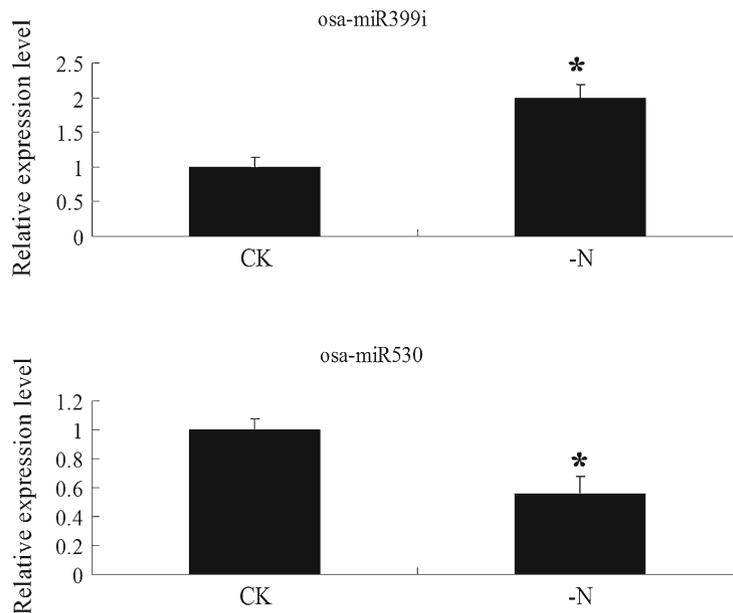
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Supplementary material



Supplementary figure 1. Number of significantly changed transcripts detected from the microarray experiment. (A) The number of specific changed and overlapped transcripts in root at 1h (NR1-CR1), 24h (NR2-CR2) and 7d (NR3-CR3) after N starvation; (B) The number of specific changed and overlapped transcripts in shoot at 1h (NS1-CS1), 24h (NS2-CS2) and 7d (NS3-CS3) after N starvation; (C) The number of specific changed and overlapped transcripts in root (Root-N) and shoot (Shoot-N) during N starvation.



Supplementary figure 2. Relative expression analysis of *osa-miR399i* and *osa-miR530* in rice plant by qRT-PCR. CK: no N starvation treatment; -N: 7d after N starvation. Y-axis means the relative expression levels, values are mean \pm SD from three independent biological replicates. * Significant differences at the level of $P = 0.05$.

Supplementary table 1. All transcripts differentially expressed in at least one time point and tissues (highlighted cell indicate significantly changing in corresponding condition, false-positive predictions by RankProd (PFP) <0.05)

Supplementary table 2A. GO enrichment analyses of the biological process of significantly changed genes in each condition

Supplementary table 2B. GO enrichment analyses of the molecular function of significantly changed genes in each condition

Supplementary table 2C. GO enrichment analyses of the cellular component of significantly changed genes in each condition

Supplementary table 3. All 2,853 putative orthologous gene pairs between rice and Arabidopsis and their responses towards N starvation stress. These genes showed differential expression in at least one treatment and one species. Cell colored in magenta represents up-regulated in corresponding treatment while cell colored in green represents down-regulated. Numbers in the cells are log₂ transformed. 1h: 1 hour, 24h: 24 hours, 7d: 7 days, 3w: 3 weeks

Supplementary table 4. 73 putative orthologous gene groups between rice and Arabidopsis and their responses towards N starvation stress. Genes differentially expressed in root after 7 days N starvation in rice were compared with genes differentially expressed in root after ten days N starvation and 20min N inducement in *Arabidopsis* (Wang R *et al.* 2003 *Plant Physiol.* **132** 556-567)

Supplementary table 5A. 7 days under N starvation vs full nutrient condition. SAM results of all 28 detectable putative rice miRNA genes in the miRNA microarray. miRNA genes with maximum signal value in all samples less than 9.96 (log₂ (1000)) were filtered out before SAM analyses. The details of format of the SAM results could be found at "Format of the Significant gene list" section of SAM users guide (<http://www-stat.stanford.edu/~tibs/SAM/sam.pdf>)

Supplementary table 5B. Target genes of osa-miR399 and osa-miR530. The potential targets were predicted by the program of miRU: Plant microRNA Potential Target Finder at <http://bioinfo3.noble.org/miRNA/miRU.htm>

Supplementary table 5C. Target genes of osa-miR399 and osa-miR530 and their expression details under N starvation. The potential targets were predicted by the program of miRU: Plant microRNA Potential Target Finder at <http://bioinfo3.noble.org/miRNA/miRU.htm>. Genes not presented on the microarray or expression level under detectable threshold are not shown

Supplementary table 6. Primers used in real-time PCR for relative expression analysis of osa-miR399i and osa-miR530 and their predicted target genes